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IIA1 V_H (SEQ ID NO: 1):
QVQLKESGPGLVAPSQSLSITCTISGFSLTDYGVHWVRQPPGKGLEWLVVIWSDGSSTYNSALKSRMTI
RKDNSKSQVFLIMNSLQTDDSAMYYCARHGTYYGMTTTGDALDYWGQGTSVTVSS

V_H 1.0 (SEQ ID NO: 2):
QVQLVESGPGLVQPGGSLRISCAISGFSLTDYGVHWVRQAPGKGLEWLVVIWSDGSSTYNSALKSRMT
ISKDNSKSTVYLQMNSLRAEDTAMYYCARHGTYYGMTTTGDALDYWGQGTLVTVSS

V_H 2.0 (SEQ ID NO: 3):
EVQLVESGGGLVQPGGSLRISCAISGFSLTDYGVHWVRQAPGKGLEWLVVIWSDGSSTYNSALKSRMT
ISKDNSKNTVYLQMNSLRAEDTAVYYCARHGTYYGMTTTGDALDYWGQGTLVTVSS

V_H 3.0 (SEQ ID NO: 4):
EVQLVESGGGLVQPGGSLRLSCAASGFSLTDYGVHWVRQAPGKGLEWVSVIWSDGSSTYNSALKSRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCARHGTYYGMTTTGDALDYWGQGTLVTVSS

V_H 4.0 (SEQ ID NO: 5):
EVQLVESGGGLVQPGGSLRLSCAISGFSLTDYGVHWVRQAPGKGLEWLVVIWSDGSSTYNSALKSRM
TISKDNSKSTVYLQMNSLRAEDTAVYYCARHGTYYGMTTTGDALDYWGQGTLVTVSS

V_H 5.0 (SEQ ID NO: 6):
QVQLVESGGGLVQPGGSLRISCAISGFSLTDYGVHWVRQAPGKGLEWLVVIWSDGSSTYNSALKSRMT
ISKDNSKSTVYLQMNSLRAEDTAMYYCARHGTYYGMTTTGDALDYWGQGTLVTVSS

IIA1 V_L (SEQ ID NO: 7):
QIVLTQSPAIMSASLGERVTMTCTASSSVSSNYLHWYQQKPGSAPNLWIYSTSNLASGVPARFSGSGSG
TSYSLTISSMEAEDAATYYCHQYLRSPPTFGGGTKLEIKR

V_L 1.0 (SEQ ID NO: 8):
DIQLTQSPSSMSASLGDRVTMTCTASSSVSSNYLHWYQQKPGKAPNLWIYSTSNLASGVPSRFSGSGSG
TDYTLTISSMQPEDFATYYCHQYLRSPPTFGQGTKLEIKR

V_L 2.0 (SEQ ID NO: 9):
DIQLTQSPSSLSASVGDRVTMTCTASSSVSSNYLHWYQQKPGKAPKLWIYSTSNLASGVPSRFSGSGSG
TDYTLTISSMQPEDFATYYCHQYLRSPPTFGQGTKLEIKR

V_L 3.0 (SEQ ID NO: 10):
DIQMTQSPSSLSASVGDRVTITCTASSSVSSNYLHWYQQKPGKAPKLLIYSTSNLASGVPSRFSGSGSGT
DFTLTISSLQPEDFATYYCHQYLRSPPTFGQGTKVEIKR

V_L 4.0 (SEQ ID NO: 11):
DIQLTQSPSSLSASVGDRVTITCTASSSVSSNYLHWYQQKPGKAPKLWIYSTSNLASGVPSRFSGSGSGT
DYTLTISSLQPEDFATYYCHQYLRSPPTFGQGTKVEIKR

V_L 5.0 (SEQ ID NO: 12):
DIQLTQSPSSLSASVGDRVTMTCTASSSVSSNYLHWYQQKPGKAPKLWIYSTSNLASGVPSRFSGSGSG
TDYTLTISSLQPEDFATYYCHQYLRSPPTFGQGTKVEIKR

FIGURE 1

	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
IIA1 V_H	QVQLKESGPGLVAPSQSLSITCTIS	GFSLTDYGVH	WVRQPPGKGLEWLV	VIWSDGSSTYNSALKS	RMTIRKDNSKSQVFLIMNSLQTDDSAMYYCAR	HGTYYGMTTTGDALDY	WGQGTSVTVSS
V_H 1.0	QVQLVESGPGLVQPGGSLRISCAIS	GFSLTDYGVH	WVRQAPGKGLEWLV	VIWSDGSSTYNSALKS	RMTISKDNSKSTVYLQMNSLRAEDTAMYYCAR	HGTYYGMTTTGDALDY	WGQGTLVTVSS
V_H 2.0	EVQLVESGGGLVQPGGSLRISCAIS	GFSLTDYGVH	WVRQAPGKGLEWLV	VIWSDGSSTYNSALKS	RMTISKDNSKNTVYLQMNSLRAEDTAVYYCAR	HGTYYGMTTTGDALDY	WGQGTLVTVSS
V_H 3.0	EVQLVESGGGLVQPGGSLRLSCAAS	GFSLTDYGVH	WVRQAPGKGLEWVS	VIWSDGSSTYNSALKS	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	HGTYYGMTTTGDALDY	WGQGTLVTVSS
V_H 4.0	EVQLVESGGGLVQPGGSLRLSCAIS	GFSLTDYGVH	WVRQAPGKGLEWLV	VIWSDGSSTYNSALKS	RMTISKDNSKSTVYLQMNSLRAEDTAVYYCAR	HGTYYGMTTTGDALDY	WGQGTLVTVSS
V_H 5.0	QVQLVESGGGLVQPGGSLRISCAIS	GFSLTDYGVH	WVRQAPGKGLEWLV	VIWSDGSSTYNSALKS	RMTISKDNSKSTVYLQMNSLRAEDTAMYYCAR	HGTYYGMTTTGDALDY	WGQGTLVTVSS

	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
IIA1 V_L	QIVLTQSPAIMSASLGERVTMTC	TASSSVSSNYLH	WYQQKPGSAPNLWIY	STSNLAS	GVPARFSGSGSGTSYSLTISSMEAEDAATYYC	HQYLRSPPT	FGGGTKLEIKR
V_L 1.0	DIQLTQSPSSMSASLGDRVTMTC	TASSSVSSNYLH	WYQQKPGKAPNLWIY	STSNLAS	GVPSRFSGSGSGTDYTLTISSMQPEDFATYYC	HQYLRSPPT	FGQGTKLEIKR
V_L 2.0	DIQLTQSPSSLSASVGDRVTMTC	TASSSVSSNYLH	WYQQKPGKAPKLWIY	STSNLAS	GVPSRFSGSGSGTDYTLTISSMQPEDFATYYC	HQYLRSPPT	FGQGTKLEIKR
V_L 3.0	DIQMTQSPSSLSASVGDRVTITC	TASSSVSSNYLH	WYQQKPGKAPKLLIY	STSNLAS	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	HQYLRSPPT	FGQGTKVEIKR
V_L 4.0	DIQLTQSPSSLSASVGDRVTITC	TASSSVSSNYLH	WYQQKPGKAPKLWIY	STSNLAS	GVPSRFSGSGSGTDYTLTISSLQPEDFATYYC	HQYLRSPPT	FGQGTKVEIKR
V_L 5.0	DIQLTQSPSSLSASVGDRVTMTC	TASSSVSSNYLH	WYQQKPGKAPKLWIY	STSNLAS	GVPSRFSGSGSGTDYTLTISSLQPEDFATYYC	HQYLRSPPT	FGQGTKVEIKR

FIGURE 2

A. IIA1 V_H sequences
[NA, SEQ ID NO: 13; AA, SEQ ID NO: 1]

```
1    ATGGCTGTCCTGGGGCTGCTTCTCTGCCTGGTGACTTTCCCAAGCTGTGTCCTGTCCCAG
      M  A  V  L  G  L  L  L  C  L  V  T  F  P  S  C  V  L  S  Q
61   GTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACA
      V  Q  L  K  E  S  G  P  G  L  V  A  P  S  Q  S  L  S  I  T
121  TGCACCATCTCAGGGTTCTCATTAACCGACTATGGTGTTCACTGGGTTCGCCAGCCTCCA
      C  T  I  S  G  F  S  L  T  D  Y  G  V  H  W  V  R  Q  P  P
181  GGAAAGGGTCTGGAGTGGCTGGTAGTGATTTGGAGTGATGGAAGCTCAACCTATAATTCA
      G  K  G  L  E  W  L  V  V  I  W  S  D  G  S  S  T  Y  N  S
241  GCTCTCAAATCCAGAATGACCATCAGGAAGGACAACTCCAAGAGCCAAGTTTTCTTAATA
      A  L  K  S  R  M  T  I  R  K  D  N  S  K  S  Q  V  F  L  I
301  ATGAACAGTCTCCAAACTGATGACTCAGCCATGTACTACTGTGCCAGACATGGAACTTAC
      M  N  S  L  Q  T  D  D  S  A  M  Y  Y  C  A  R  H  G  T  Y
361  TACGGTATGACTACGACGGGGGATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACC
      Y  G  M  T  T  T  G  D  A  L  D  Y  W  G  Q  G  T  S  V  T
421  GTCTCCTCA
      V  S  S
```

B. IIA1 V_L sequences
[NA, SEQ ID NO: 14; AA, SEQ ID NO: 7]

```
1    ATGGATTTTCAGGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATAATGTCC
      M  D  F  Q  V  Q  I  F  S  F  L  L  I  S  A  S  V  I  M  S
61   AGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCTAGGGGAACGG
      R  G  Q  I  V  L  T  Q  S  P  A  I  M  S  A  S  L  G  E  R
121  GTCACCATGACCTGCACTGCCAGTTCAAGTGTAAGTTCCAATTACTTGCACTGGTACCAG
      V  T  M  T  C  T  A  S  S  S  V  S  S  N  Y  L  H  W  Y  Q
181  CAGAAGCCAGGATCCGCCCCCAATCTCTGGATTTATAGCACATCCAACCTGGCTTCTGGA
      Q  K  P  G  S  A  P  N  L  W  I  Y  S  T  S  N  L  A  S  G
241  GTCCCAGCTCGTTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGC
      V  P  A  R  F  S  G  S  G  S  G  T  S  Y  S  L  T  I  S  S
301  ATGGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCTTCGTTCCCCACCGACG
      M  E  A  E  D  A  A  T  Y  Y  C  H  Q  Y  L  R  S  P  P  T
361  TTCGGTGGAGGCACCAAGCTGGAAATCAAA
      F  G  G  G  T  K  L  E  I  K
```

FIGURE 3

A. Antibody 200-4 V_H sequences
[NA, SEQ ID NO: 15; AA, SEQ ID NO: 16]

```
1    ATGGCTGTCCTGGGGCTGCTTCTCTGCCTGGTGACTTTCCCAAGCTGTGTCCTGTCCCAG
      M  A  V  L  G  L  L  L  C  L  V  T  F  P  S  C  V  L  S  Q
61   GTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACA
      V  Q  L  K  E  S  G  P  G  L  V  A  P  S  Q  S  L  S  I  T
121  TGCACCATCTCAGGGTTCTCATTAACCGACTATGGTGTTCACTGGGTTCGCCAGCCTCCA
      C  T  I  S  G  F  S  L  T  D  Y  G  V  H  W  V  R  Q  P  P
181  GGAAAGGGTCTGGAGTGGCTGGTAGTGATTTGGAGTGATGGAAGCTCAACCTATAATTCA
      G  K  G  L  E  W  L  V  V  I  W  S  D  G  S  S  T  Y  N  S
241  GCTCTCAAATCCAGAATGACCATCAGGAAGGACAACTCCAAGAGCCAAGTTTTCTTAATA
      A  L  K  S  R  M  T  I  R  K  D  N  S  K  S  Q  V  F  L  I
301  ATGAACAGTCTCCAAACTGATGACTCAGCCATGTACTACTGTGCCAGACATGGAACTTAC
      M  N  S  L  Q  T  D  D  S  A  M  Y  Y  C  A  R  H  G  T  Y
361  TACGGTATGACTACGACGGGGGATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCACC
      Y  G  M  T  T  T  G  D  A  L  D  Y  W  G  Q  G  T  S  V  T
421  GTCTCGAGC
      V  S  S
```

B. Antibody 200-4 V_L sequences
[NA, SEQ ID NO: 17; AA, SEQ ID NO: 18]

```
1    ATGGATTTTCAGGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCCTCAGTCATAATGTCC
      M  D  F  Q  V  Q  I  F  S  F  L  L  I  S  A  S  V  I  M  S
61   AGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCTAGGGGAACGG
      R  G  Q  I  V  L  T  Q  S  P  A  I  M  S  A  S  L  G  E  R
121  GTCACCATGACCTGCACTGCCAGTTCAAGTGTAAGTTCCAATTACTTGCACTGGTACCAG
      V  T  M  T  C  T  A  S  S  S  V  S  S  N  Y  L  H  W  Y  Q
181  CAGAAGCCAGGATCCGCCCCCAATCTCTGGATTTATAGCACATCCAACCTGGCTTCTGGA
      Q  K  P  G  S  A  P  N  L  W  I  Y  S  T  S  N  L  A  S  G
241  GTCCCAGCTCGTTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGC
      V  P  A  R  F  S  G  S  G  S  G  T  S  Y  S  L  T  I  S  S
301  ATGGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCTTCGTTCCCCACCGACG
      M  E  A  E  D  A  A  T  Y  Y  C  H  Q  Y  L  R  S  P  P  T
361  TTCGGTGGAGGCACCAAGCTCGAGATCAAA
      F  G  G  G  T  K  L  E  I  K
```

FIGURE 4

A. M200 V_H sequences
[NA, SEQ ID NO: 19; AA, SEQ ID NO: 20]

```
   1  TCTAGACCACCATGGCTGTCCTGGGGCTGCTTCTCTGCCTGGTGACTTTCCCAAGCTGTG
                 M  A  V  L  G  L  L  L  C  L  V  T  F  P  S  C
  61  TCCTGTCCCAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCC
      V  L  S  Q  V  Q  L  K  E  S  G  P  G  L  V  A  P  S  Q  S
 121  TGTCCATCACATGCACCATCTCAGGGTTCTCATTAACCGACTATGGTGTTCACTGGGTTC
      L  S  I  T  C  T  I  S  G  F  S  L  T  D  Y  G  V  H  W  V
 181  GCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGTAGTGATTTGGAGTGATGGAAGCTCAA
      R  Q  P  P  G  K  G  L  E  W  L  V  V  I  W  S  D  G  S  S
 241  CCTATAATTCAGCTCTCAAATCCAGAATGACCATCAGGAAGGACAACTCCAAGAGCCAAG
      T  Y  N  S  A  L  K  S  R  M  T  I  R  K  D  N  S  K  S  Q
 301  TTTTCTTAATAATGAACAGTCTCCAAACTGATGACTCAGCCATGTACTACTGTGCCAGAC
      V  F  L  I  M  N  S  L  Q  T  D  D  S  A  M  Y  Y  C  A  R
 361  ATGGAACTTACTACGGAATGACTACGACGGGGGATGCTTTGGACTACTGGGGTCAAGGAA
      H  G  T  Y  Y  G  M  T  T  T  G  D  A  L  D  Y  W  G  Q  G
 421  CCTCAGTCACCGTCTCCTCAG^GTAAGAATGGCCTCTAGA
      T  S  V  T  V  S  S
```

B. M200 V_L sequences
[NA, SEQ ID NO: 21; AA, SEQ ID NO: 22]

```
   1  ACGCGTCCACCATGGATTTTCAGGTGCAGATTTTCAGCTTCCTGCTAATCAGTGCCTCAG
                 M  D  F  Q  V  Q  I  F  S  F  L  L  I  S  A  S
  61  TCATAATGTCCAGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTC
      V  I  M  S  R  G  Q  I  V  L  T  Q  S  P  A  I  M  S  A  S
 121  TAGGGGAACGGGTCACCATGACCTGCACTGCCAGTTCAAGTGTCAGTTCCAATTACTTGC
      L  G  E  R  V  T  M  T  C  T  A  S  S  S  V  S  S  N  Y  L
 181  ACTGGTACCAGCAGAAGCCAGGATCCGCCCCCAATCTCTGGATTTATAGCACATCCAACC
      H  W  Y  Q  Q  K  P  G  S  A  P  N  L  W  I  Y  S  T  S  N
 241  TGGCTTCTGGAGTCCCAGCTCGTTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCA
      L  A  S  G  V  P  A  R  F  S  G  S  G  S  G  T  S  Y  S  L
 301  CAATCAGCAGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCTTCGTT
      T  I  S  S  M  E  A  E  D  A  A  T  Y  Y  C  H  Q  Y  L  R
 361  CCCCACCGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAAC^GTAAGTAGAATCCAAAGT
      S  P  P  T  F  G  G  G  T  K  L  E  I  K
 421  CTAGA
```

FIGURE 5

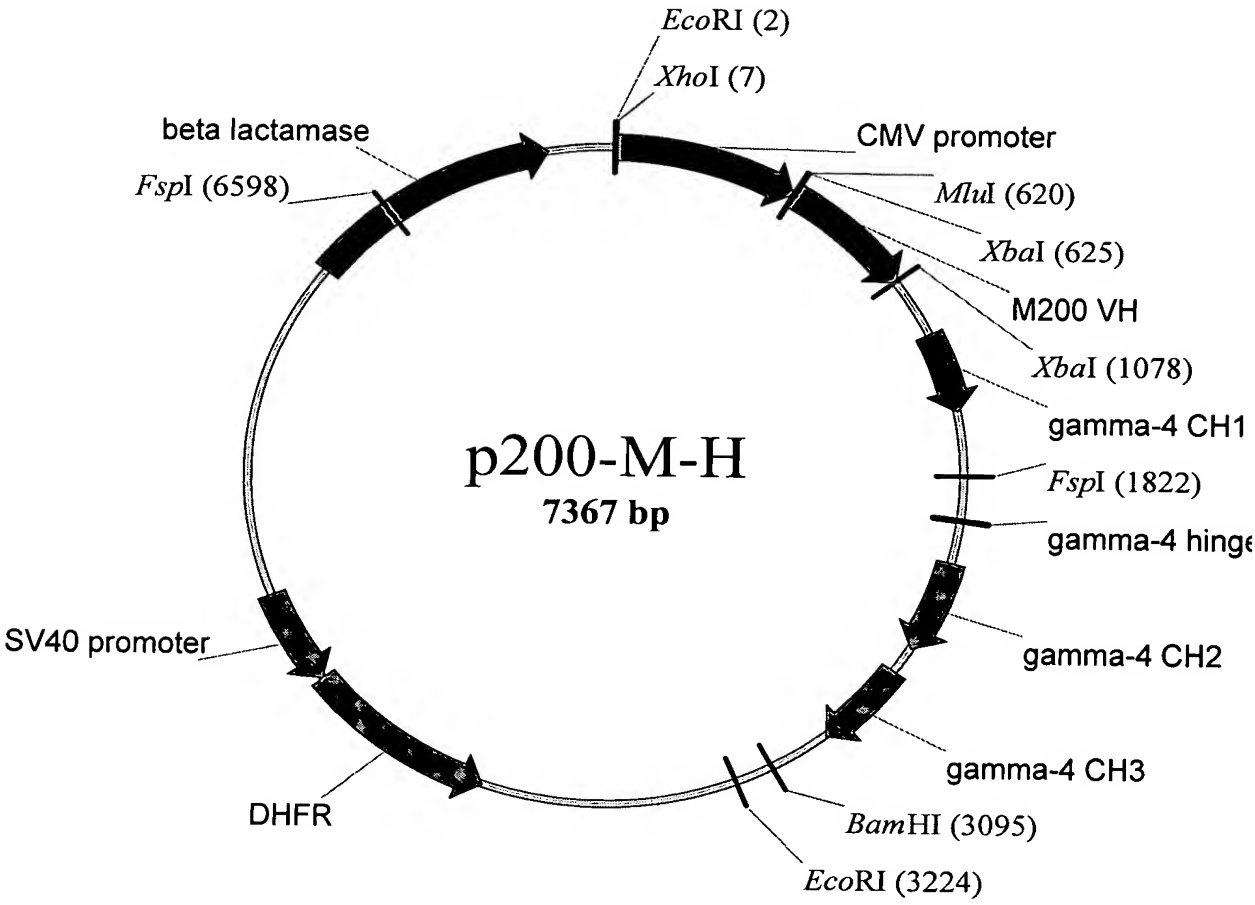

EcoRI (2)
XhoI (7)
beta lactamase
CMV promoter
FspI (6598)
MluI (620)
XbaI (625)
M200 VH
XbaI (1078)
gamma-4 CH1
p200-M-H
7367 bp
FspI (1822)
gamma-4 hinge
SV40 promoter
gamma-4 CH2
gamma-4 CH3
DHFR
BamHI (3095)
EcoRI (3224)

FIGURE 6

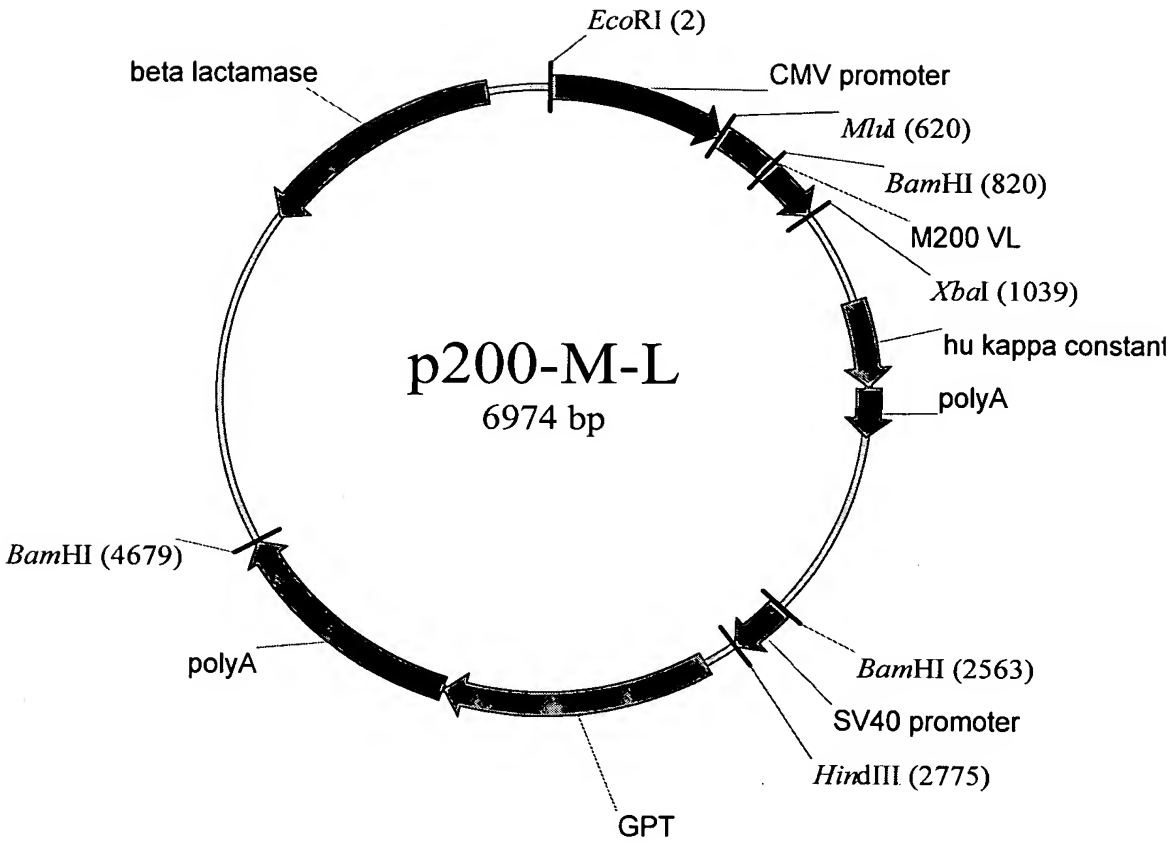

EcoRI (2)
CMV promoter
MluI (620)
BamHI (820)
M200 VL
XbaI (1039)
hu kappa constant
polyA
BamHI (2563)
SV40 promoter
HindIII (2775)
GPT
polyA
BamHI (4679)
beta lactamase
p200-M-L
6974 bp

FIGURE 7

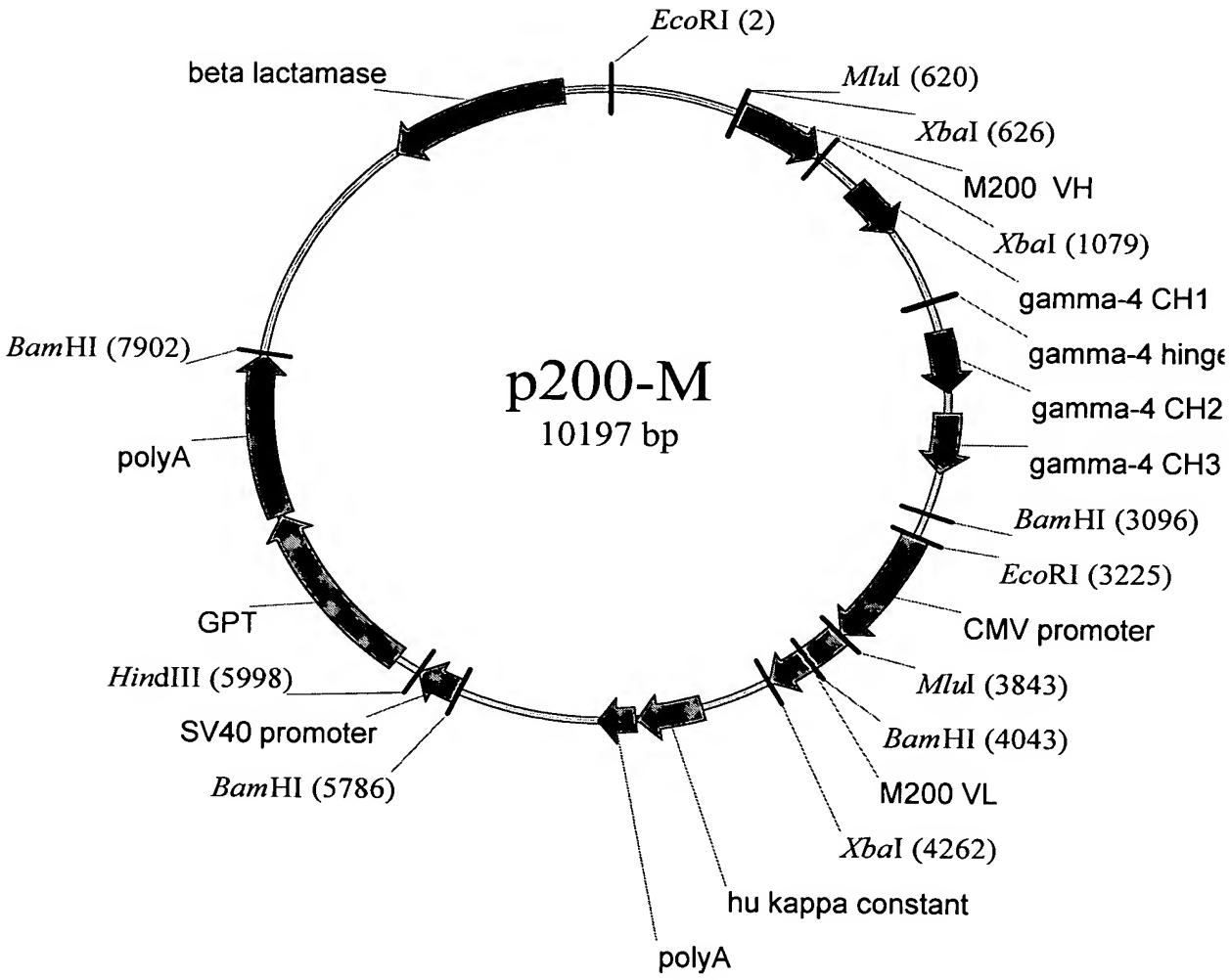

EcoRI (2)
beta lactamase
MluI (620)
XbaI (626)
M200 VH
XbaI (1079)
gamma-4 CH1
gamma-4 hinge
gamma-4 CH2
gamma-4 CH3
BamHI (3096)
EcoRI (3225)
CMV promoter
MluI (3843)
BamHI (4043)
M200 VL
XbaI (4262)
hu kappa constant
polyA
BamHI (5786)
SV40 promoter
HindIII (5998)
GPT
polyA
BamHI (7902)
p200-M
10197 bp

FIGURE 8

M200 COMPLETE HEAVY CHAIN DNA SEQUENCE
(SEQ ID NO: 23)

CAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCC
ATCACATGCACCATCTCAGGGTTCTCATTAACCGACTATGGTGTTCACTGGGTTCGC
CAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGTAGTGATTTGGAGTGATGGAAGCTCA
ACCTATAATTCAGCTCTCAAATCCAGAATGACCATCAGGAAGGACAACTCCAAGAGC
CAAGTTTTCTTAATAATGAACAGTCTCCAAACTGATGACTCAGCCATGTACTACTGT
GCCAGACATGGAACTTACTACGGAATGACTACGACGGGGGATGCTTTGGACTACTGG
GGTCAAGGAACCTCAGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTC
CCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTG
GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACC
AGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTA
GATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTCCAAATATGGTCCC
CCATGCCCATCATGCCCAGCACCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTC
CCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTG
GTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGC
GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC
CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAA
GCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAG
ATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGAC
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAG
AGCAGGTGGCAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC
AACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGGTAAA

M200 COMPLETE LIGHT CHAIN DNA SEQUENCE
(SEQ ID NO: 24)

CAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCTAGGGGAACGGGTC
ACCATGACCTGCACTGCCAGTTCAAGTGTAAGTTCCAATTACTTGCACTGGTACCAG
CAGAAGCCAGGATCCGCCCCCAATCTCTGGATTTATAGCACATCCAACCTGGCTTCT
GGAGTCCCAGCTCGTTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATC
AGCAGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCTTCGTTCC
CCACCGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGAACTGTGGCTGCACCA
TCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTT
GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGAT
AACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC
AGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACAC
AAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TTCAACAGGGGAGAGTGT

FIGURE 9

M200 COMPLETE HEAVY CHAIN AMINO ACID SEQUENCE
(SEQ ID NO: 25)

QVQLKESGPGLVAPSQSLSITCTISGFSLTDYGVHWVRQPPGKGLEWLVVIWSDGSS
TYNSALKSRMTIRKDNSKSQVFLIMNSLQTDDSAMYYCARHGTYYGMTTTGDALDYW
GQGTSVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT
SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP
PCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG
VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK
AKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

M200 COMPLETE LIGHT CHAIN AMINO ACID SEQUENCE
(SEQ ID NO: 26)

QIVLTQSPAIMSASLGERVTMTCTASSSVSSNYLHWYQQKPGSAPNLWIYSTSNLASGVP
ARFSGSGSGTSYSLTISSMEAEDAATYYCHQYLRSPPTFGGGTKLEIKRTVAAPSVFIFP
PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL
TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 10

F200 COMPLETE HEAVY CHAIN DNA SEQUENCE
(SEQ ID NO: 27)

CAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCC
ATCACATGCACCATCTCAGGGTTCTCATTAACCGACTATGGTGTTCACTGGGTTCGC
CAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGTAGTGATTTGGAGTGATGGAAGCTCA
ACCTATAATTCAGCTCTCAAATCCAGAATGACCATCAGGAAGGACAACTCCAAGAGC
CAAGTTTTCTTAATAATGAACAGTCTCCAAACTGATGACTCAGCCATGTACTACTGT
GCCAGACATGGAACTTACTACGGAATGACTACGACGGGGGATGCTTTGGACTACTGG
GGTCAAGGAACCTCAGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTC
CCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTG
GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACC
AGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTA
GATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTCCAAATATGGTCCC
CCATGCCCATCA

F200 COMPLETE HEAVY CHAIN AMINO ACID SEQUENCE
(SEQ ID NO: 28)

QVQLKESGPGLVAPSQSLSITCTISGFSLTDYGVHWVRQPPGKGLEWLVVIWSDGSS
TYNSALKSRMTIRKDNSKSQVFLIMNSLQTDDSAMYYCARHGTYYGMTTTGDALDYW
GQGTSVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT
SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP
PCPS

FIGURE 11

huM200 COMPLETE HEAVY CHAIN DNA SEQUENCE
(SEQ ID NO: 29)

GAGGTGCAGCTGGTGGAGTCAGGAGGAGGCCTGGTGCAGCCCGGAGGAAGCCTGAGA
CTGTCATGCGCCGCCTCAGGGTTCTCATTAACCGACTATGGTGTTCACTGGGTTCGC
CAGGCCCCAGGAAAGGGTCTGGAGTGGCTGGTGGTGATTTGGAGTGATGGAAGCTCA
ACCTATAATTCAGCTCTCAAATCCAGAATGACCATCTCAAAGGACAACGCCAAGAAC
ACCGTGTACTTACAGATGAACAGTCTCAGAGCTGAGGACACCGCCGTGTACTACTGT
GCCAGACATGGAACTTACTACGGAATGACTACGACGGGGGATGCTTTGGACTACTGG
GGTCAAGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTC
CCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTG
GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACC
AGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTA
GATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTCCAAATATGGTCCC
CCATGCCCATCATGCCCAGCACCTGAGTTCCTGGGGGGACCATCAGTCTTCCTGTTC
CCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTG
GTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGC
GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACGTAC
CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAA
GCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAG
ATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGAC
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAG
AGCAGGTGGCAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC
AACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGGTAAA

huM200 COMPLETE LIGHT CHAIN DNA SEQUENCE
(SEQ ID NO: 30)

GAAATTGTTCTCACCCAGTCTCCAGCAACCCTCTCTCTCTCTCCGGGGGAACGGGCT
ACCCTCTCCTGCACTGCCAGTTCAAGTGTCAGTTCCAATTACTTGCACTGGTACCAG
CAGAAGCCAGGACAGGCCCCCCGTCTCCTCATTTATAGCACATCCAACCTGGCTTCT
GGAGTCCCAGCTCGTTTCAGTGGCAGTGGGTCTGGGACCTCTTACACCCTCACAATC
AGCAGCCTCGAGCCAGAAGATTTCGCCGTCTATTACTGCCACCAGTATCTTCGTTCC
CCACCGACGTTCGGTGGAGGCACCAAGGTCGAAATCAAACGAACTGTGGCTGCACCA
TCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTT
GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGAT
AACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGAC
AGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACAC
AAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TTCAACAGGGGAGAGTGT

FIGURE 12

huM200 COMPLETE HEAVY CHAIN AMINO ACID SEQUENCE
(SEQ ID NO: 31)

EVQLVESGGGLVQPGGSLRLSCAASGFSLTDYGVHWVRQAPGKGLEWLVVIWSDGSS
TYNSALKSRMTISKDNAKNTVYLQMNSLRAEDTAVYYCARHGTYYGMTTTGDALDYW
GQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT
SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP
PCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG
VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK
AKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

huM200 COMPLETE LIGHT CHAIN AMINO ACID SEQUENCE
(SEQ ID NO: 32)

EIVLTQSPATLSLSPGERATLSCTASSSVSSNYLHWYQQKPGQAPRLLIYSTSNLASGVP
ARFSGSGSGTSYTLTISSLEPEDFAVYYCHQYLRSPPTFGGGTKVEIKRTVAAPSVFIFP
PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL
TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 13

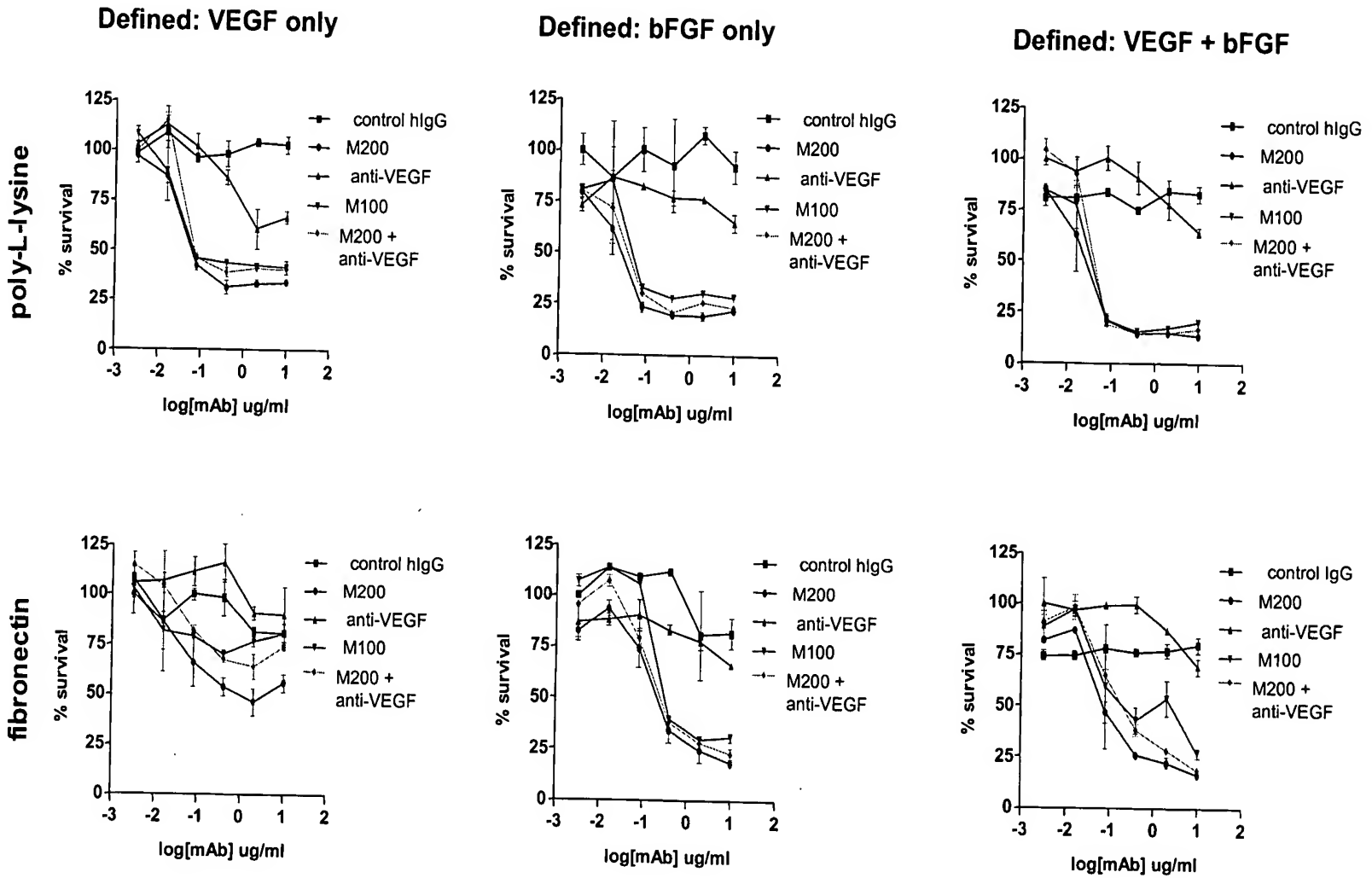
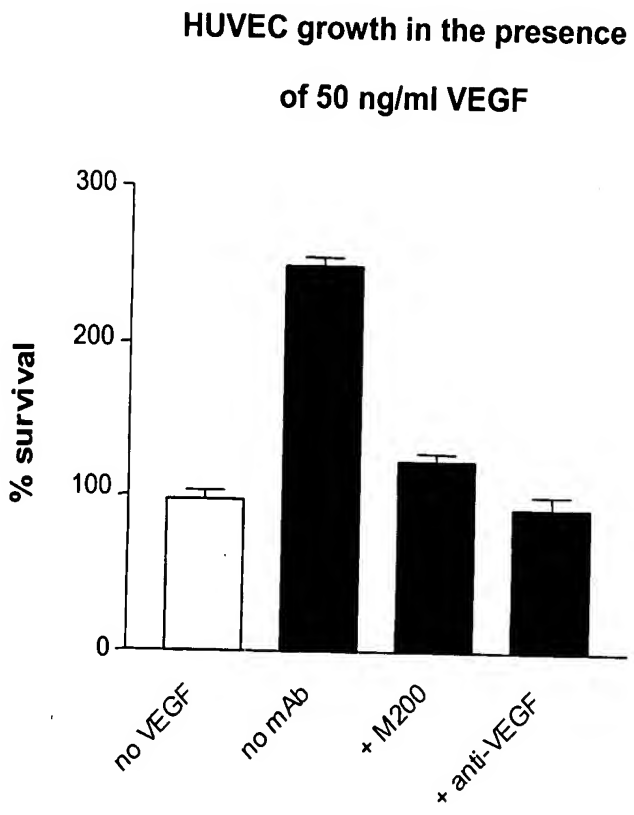

Defined: VEGF only
Defined: bFGF only
Defined: VEGF + bFGF
poly-L-lysine
fibronectin
% survival
log[mAb] ug/ml
control hIgG
control IgG
M200
anti-VEGF
M100
M200 +
anti-VEGF

FIGURE 14

A.


HUVEC growth in the presence
of 50 ng/ml VEGF
% survival
300
200
100
0
no VEGF
no mAb
+ M200
+ anti-VEGF

B.

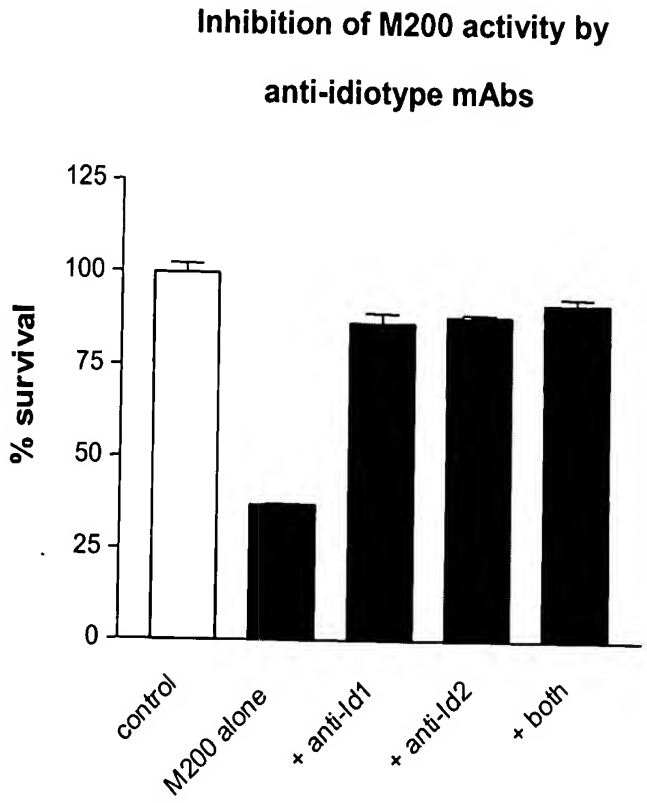
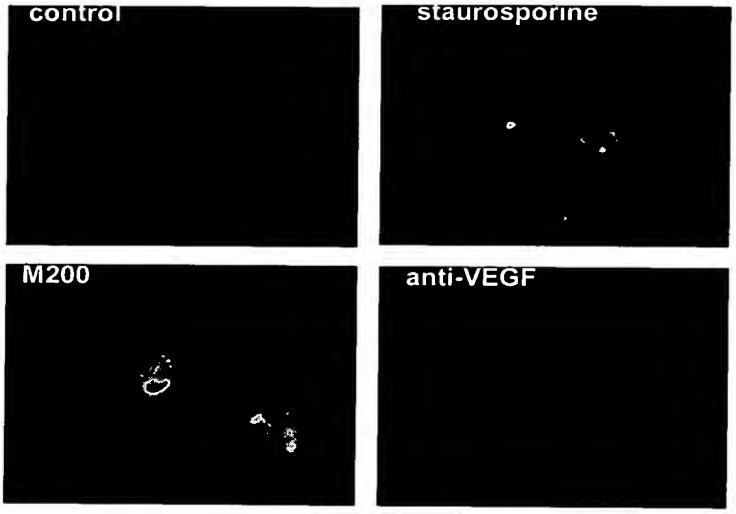

Inhibition of M200 activity by
anti-idiotype mAbs
% survival
125
100
75
50
25
0
control
M200 alone
+ anti-Id1
+ anti-Id2
+ both

FIGURE 15

A.

Visualization of Annexin V positive cells by Immunofluorescence



B.

Quantification of Annexin V positive cells by flow cytometry

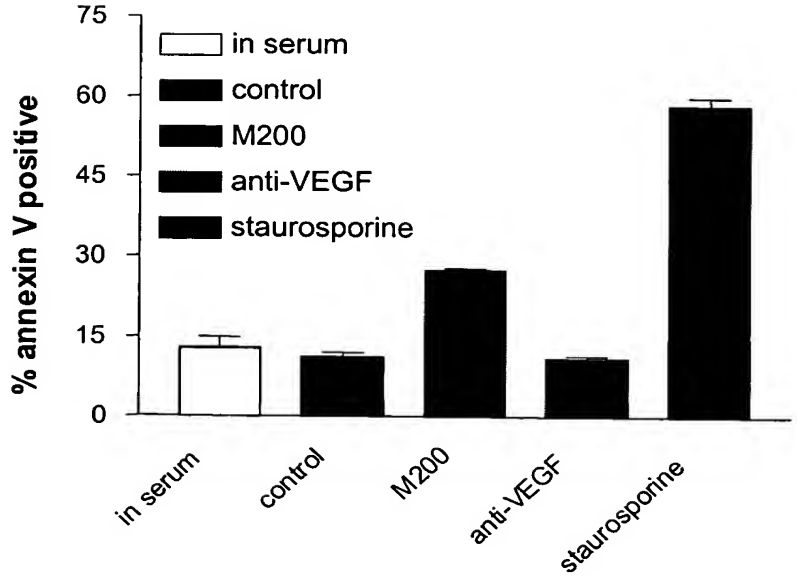


FIGURE 16

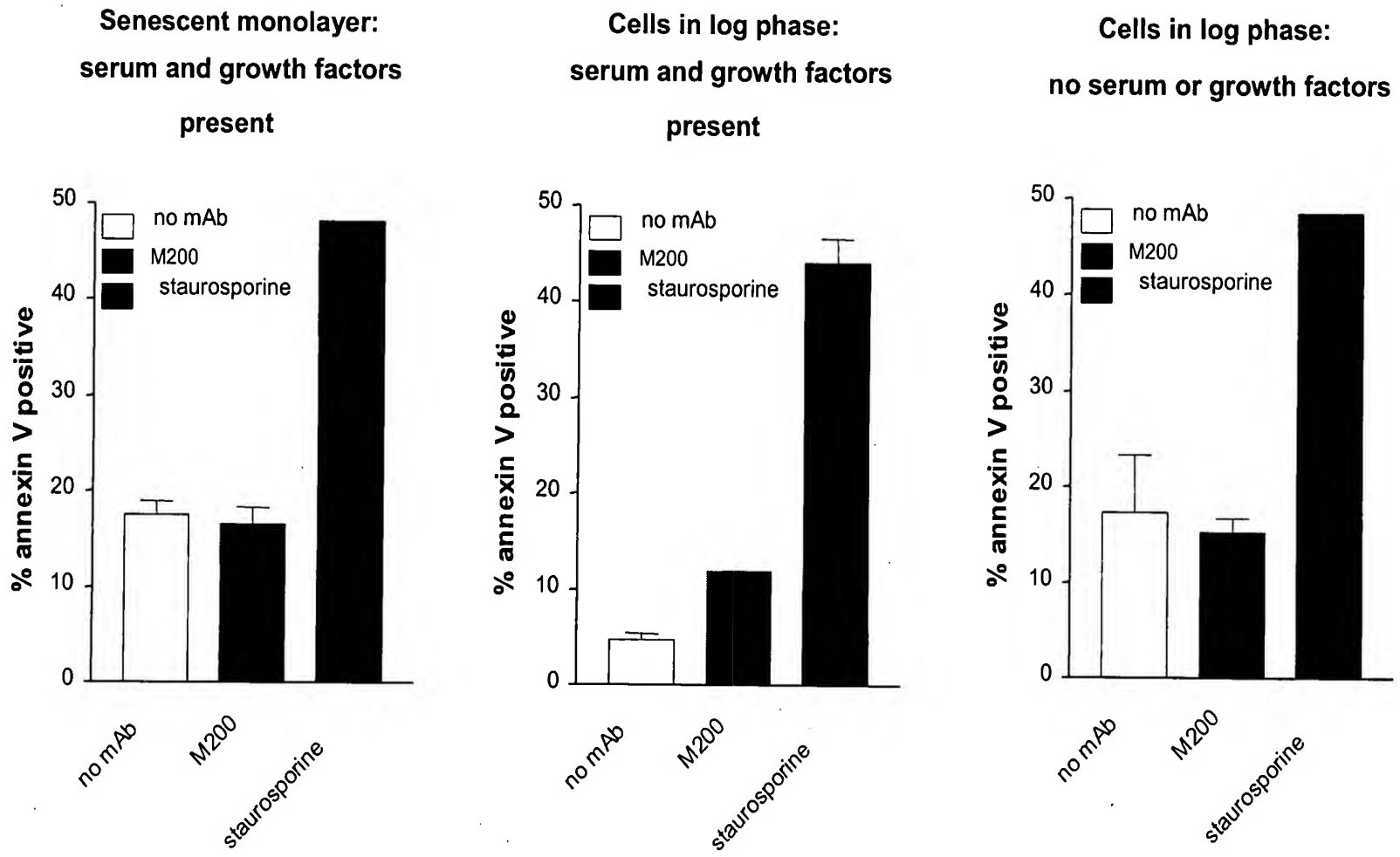
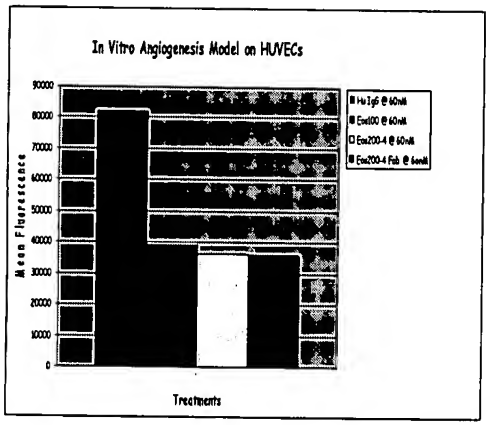
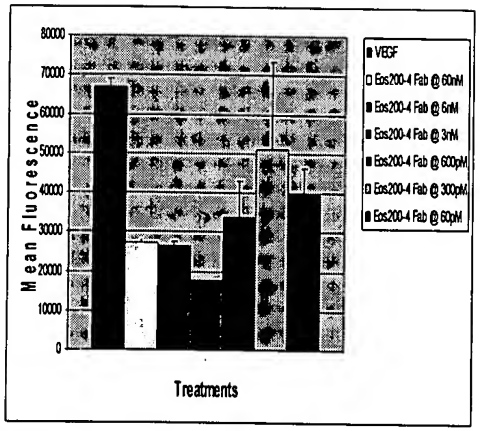
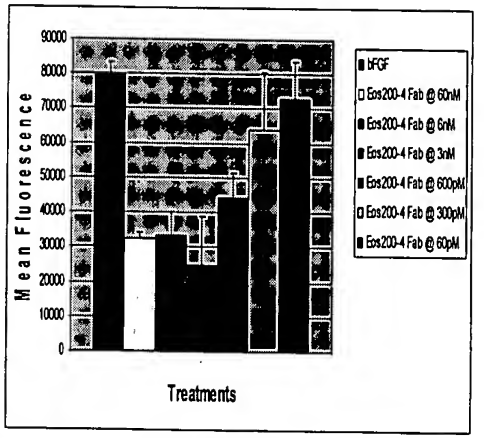
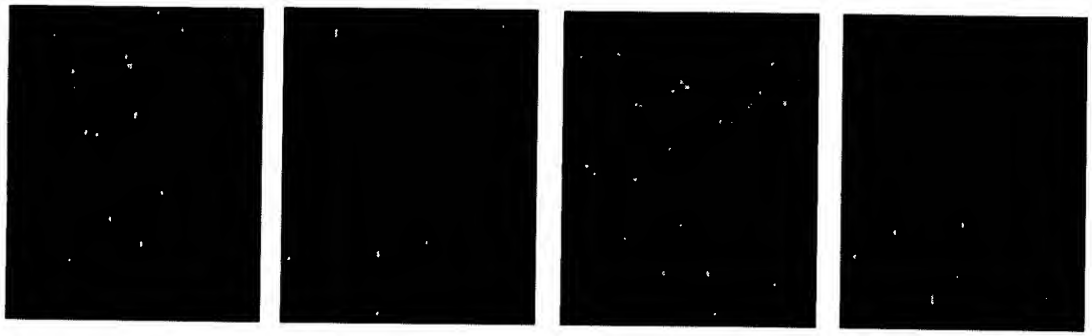

Senescent monolayer:
serum and growth factors
present
Cells in log phase:
serum and growth factors
present
Cells in log phase:
no serum or growth factors
% annexin V positive
50
40
30
20
10
0
no mAb
M200
staurosporine
no mAb
M200
staurosporine

FIGURE 17





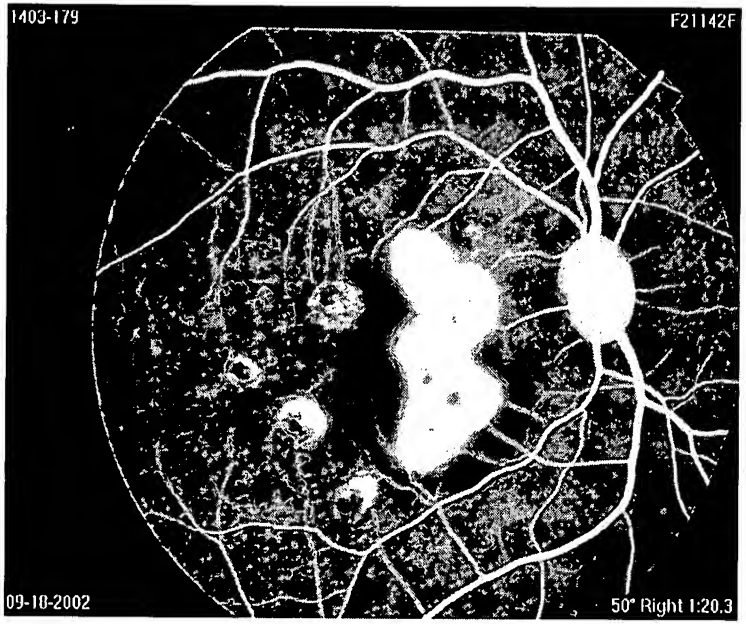




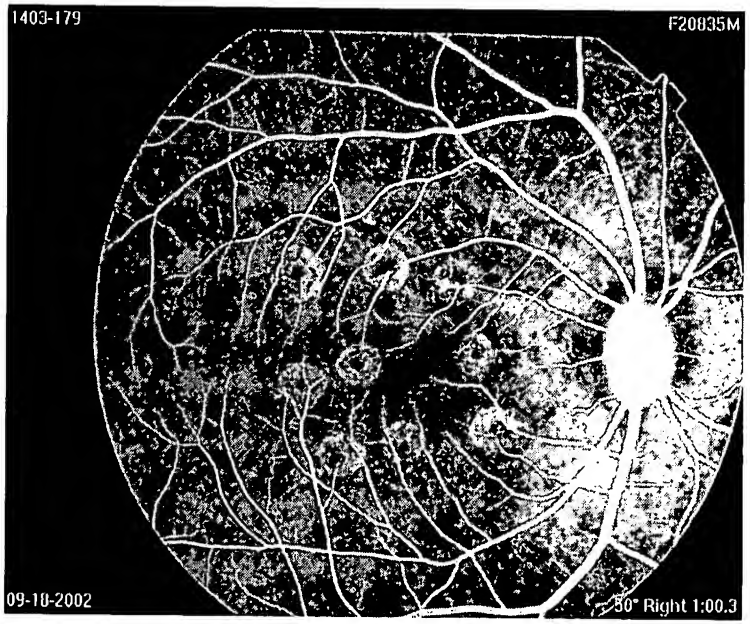
Control F200 (EOS 200-4 Fab) Control F200 (EOS 200-4 Fab) Control F200 (EOS 200-4 Fab)

A. rTGFα, VEGF and HGF added B. Only VEGF added C. Only HGF added

FIGURE 18

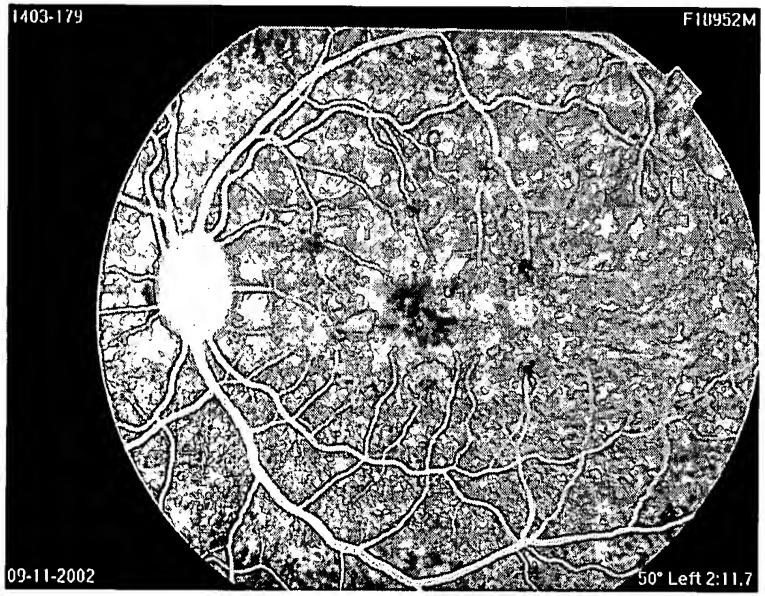


A. Control (rituxan)
Day20



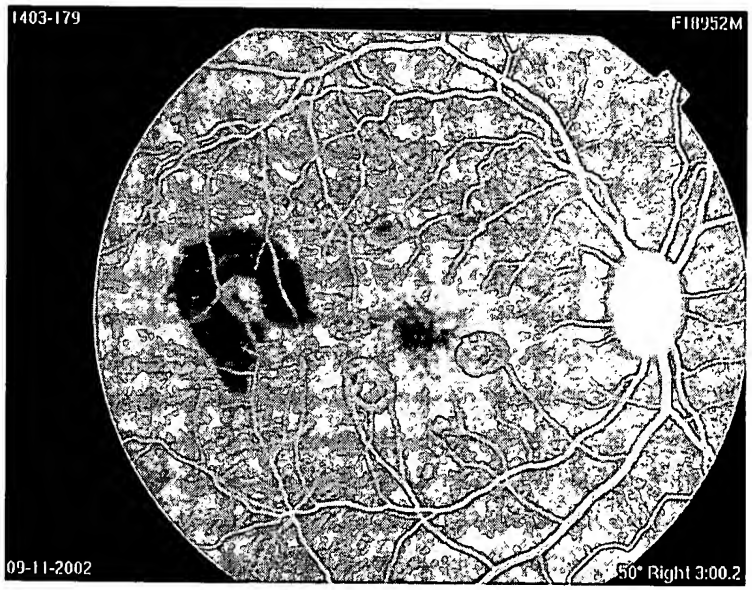
B. M200 treated
Day20

FIGURE 19



A. Control (left eye)

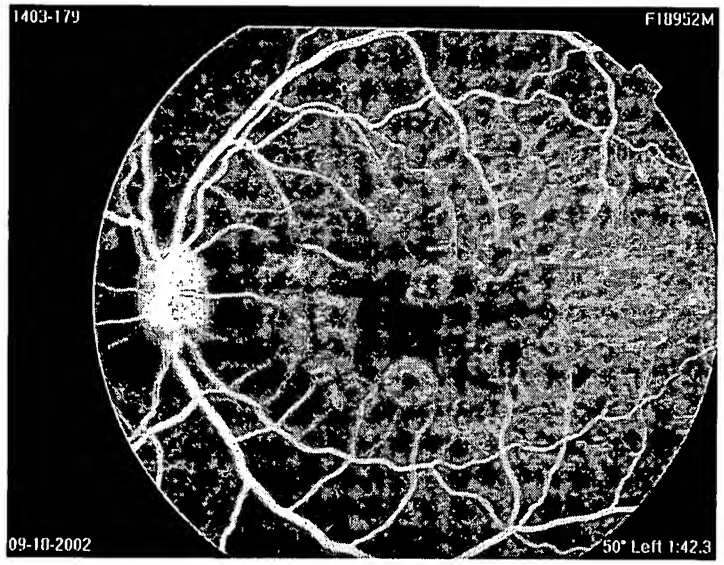
Day 13



B. M200 (right eye)

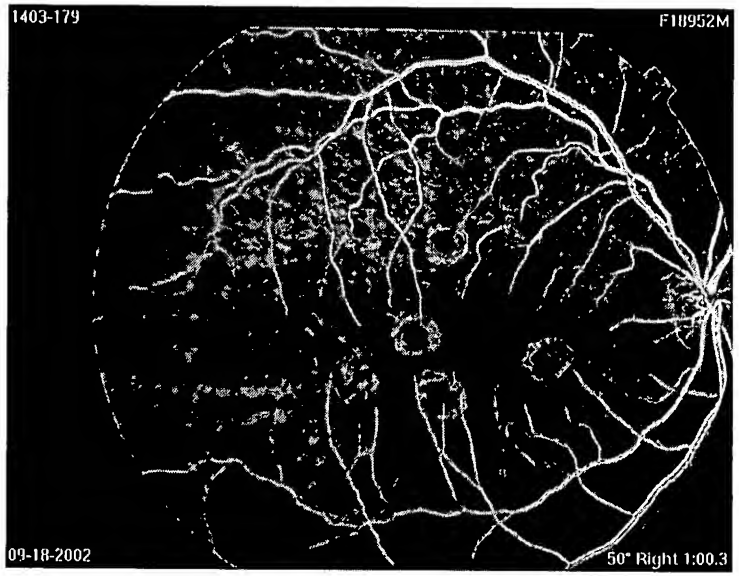
Day 13

FIGURE 20



A. Control (left eye)

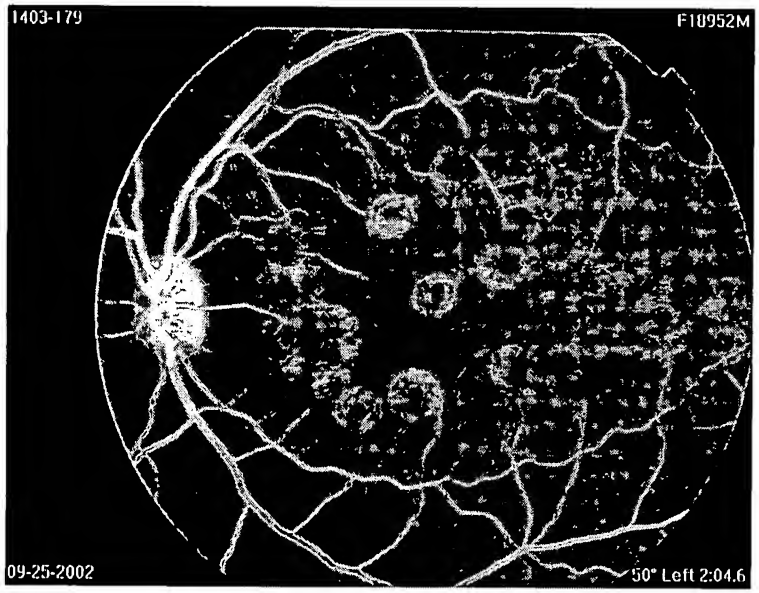
Day 20



B. M200 (right eye)

Day 20

FIGURE 21



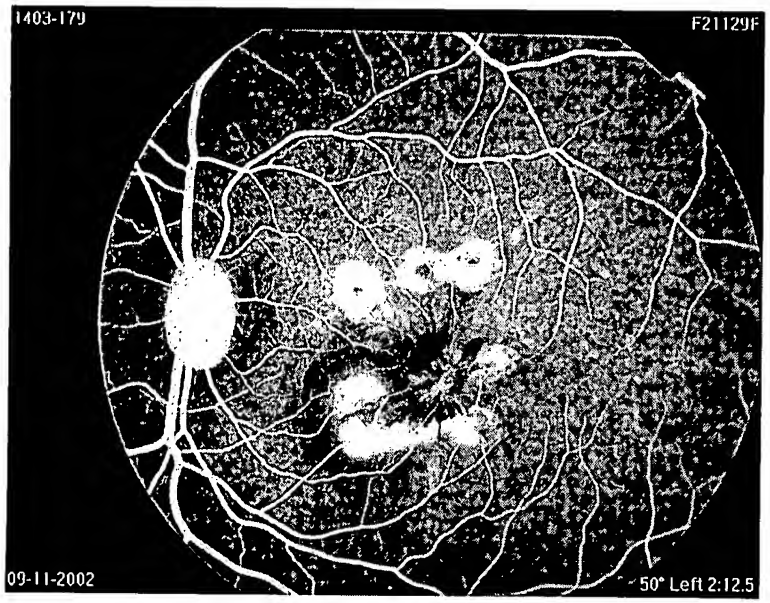
A. Control (left eye)

Day 27

B. M200 (right eye)

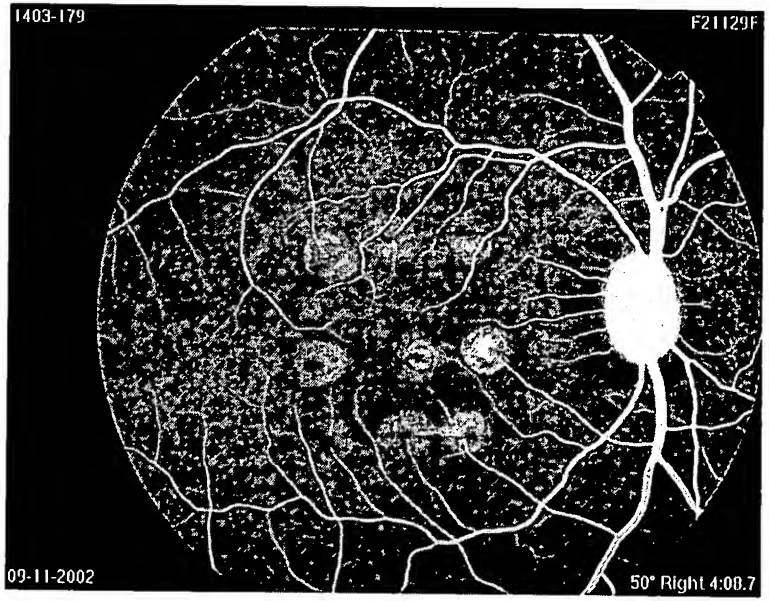
Day 27

FIGURE 22



A. Control (left eye)

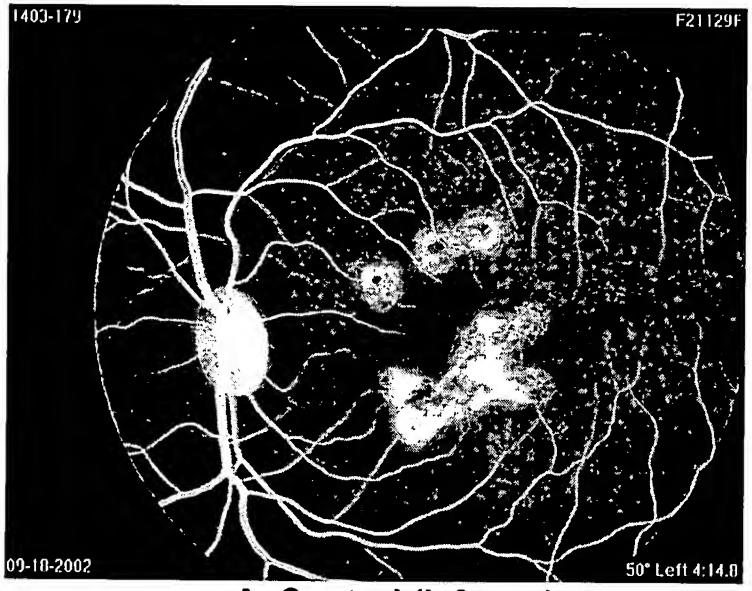
Day 13



B. F200 (right eye)

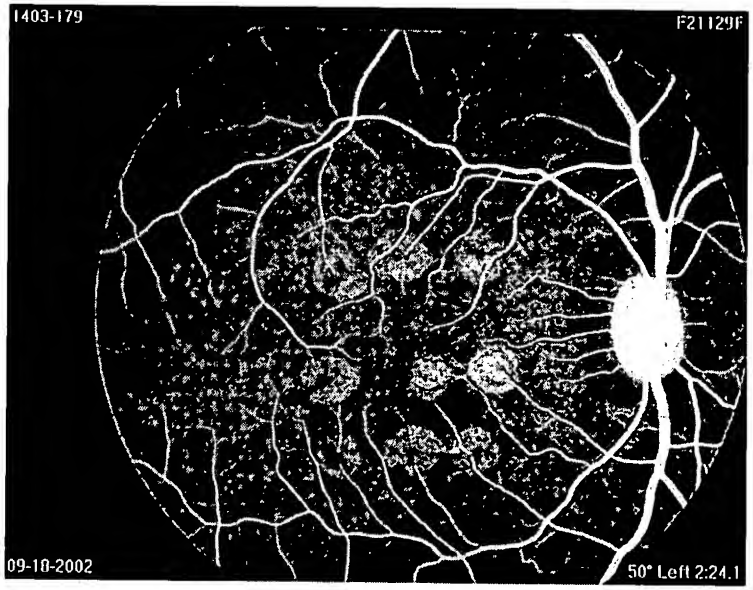
Day 13

FIGURE 23



A. Control (left eye)

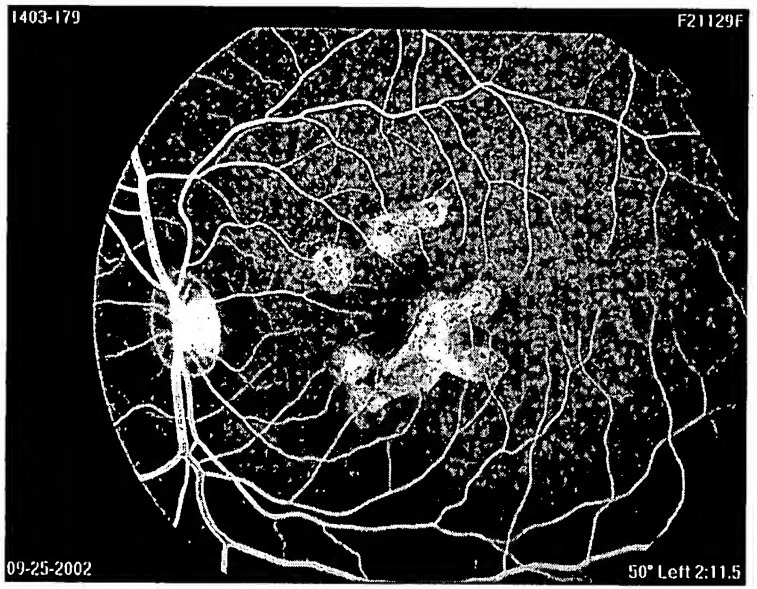
Day 20



B. F200 (right eye)

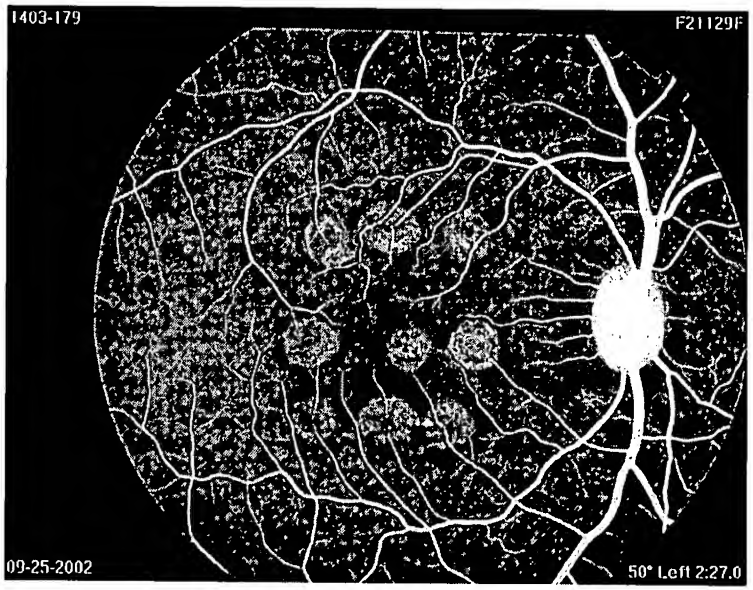
Day 20

FIGURE 24



A. Control (left eye)

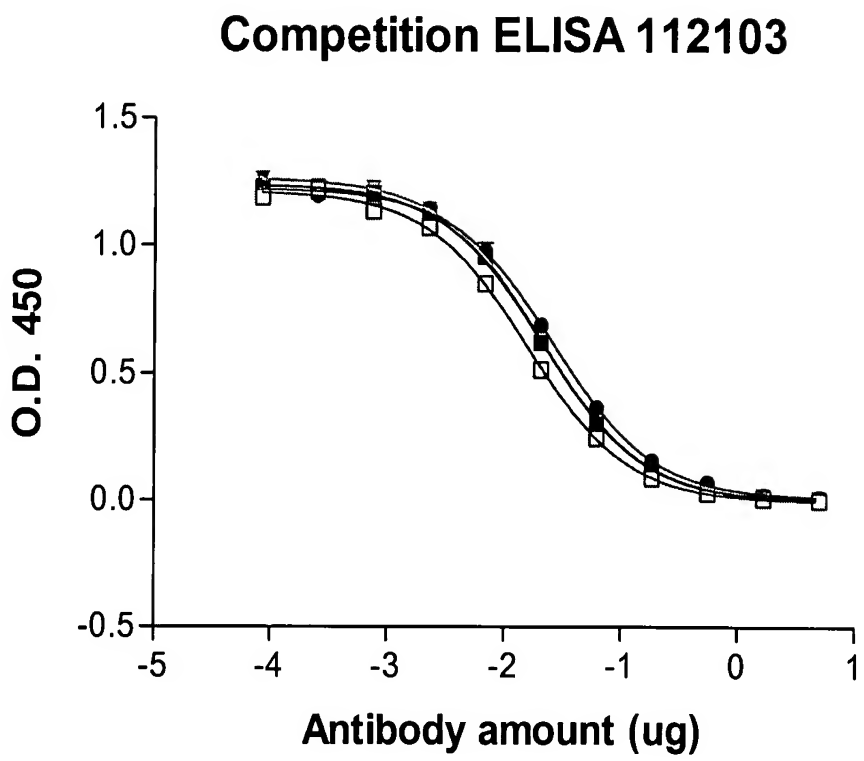
Day 27



B. F200 (right eye)

Day 27

FIGURE 25



	EC50 (ug/ml)
Mouse IIA1	79.1
200-4	106.3
huM200-G4	131.8
huM200-g2m3G	102.8

FIGURE 26